



## SEQUENCE LISTING

<110> BUJARD, Hermann  
GOSSEN, Manfred

B( <120> Transgenic Organisms Having Tetracycline-Regulated Transcriptional  
Regulatory Systems (as amended)

<130> BBI-009C3CN2

<140> 09/874389  
<141> 2001-06-04

<150> 09/161902  
<151> 1998-09-28

<150> 08/487472  
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<170> FastSEQ for Windows Version 4.0

<210> 1  
<211> 1008  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Tet activator fusion

<220>  
<221> exon  
<222> (1)...(1008)

<220>  
<221> mRNA  
<222> (1)...(1008)

<220>  
<221> misc\_binding

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&lt;222&gt; (1)...(207)

&lt;220&gt;

&lt;221&gt; misc\_binding

&lt;222&gt; (208)...(335)

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(1005)

&lt;400&gt; 1

atg tct aga tta gat aaa act aaa gtg att aac agc gca tta gag ctg	48
Met Ser Arg Leu Asp Lys Thr Lys Val Ile Asn Ser Ala Leu Glu Leu	
1 5 10 15	
ctt aat gag gtc gga atc gaa ggt tta aca acc cgt aaa ctc gcc cag	96
Leu Asn Glu Val Gly Ile Glu Gly Leu Thr Thr Arg Lys Leu Ala Gln	
20 25 30	
aag cta ggt gta gag cag cct aca ctg tat tgg cat gta aaa aat aag	144
Lys Leu Gly Val Glu Gln Pro Thr Leu Tyr Trp His Val Lys Asn Lys	
35 40 45	
cgg gct ttg ctc gac gcc tta gcc att gag atg tta gat agg cac cat	192
Arg Ala Leu Leu Asp Ala Leu Ala Ile Glu Met Leu Asp Arg His His	
50 55 60	
act cac ttt tgc cct tta aaa ggg gaa agc tgg caa gat ttt tta cgc	240
Thr His Phe Cys Pro Leu Lys Gly Glu Ser Trp Gln Asp Phe Leu Arg	
65 70 75 80	
aat aag gct aaa agt ttt aga tgt gct tta cta act cat cgc aat gga	288
Asn Lys Ala Lys Ser Phe Arg Cys Ala Leu Leu Thr His Arg Asn Gly	
85 90 95	
gca aaa gta cat tca gat aca cgg cct aca gaa aaa cag tat gaa act	336
Ala Lys Val His Ser Asp Thr Arg Pro Thr Glu Lys Gln Tyr Glu Thr	
100 105 110	
ctc gaa aat caa tta gcc ttt tta tgc caa caa ggt ttt tca cta gag	384
Leu Glu Asn Gln Leu Ala Phe Leu Cys Gln Gln Gly Phe Ser Leu Glu	
115 120 125	
aat gca tta tat gca ctc agc gct gtg ggg cat ttt act tta ggt tgc	432
Asn Ala Leu Tyr Ala Leu Ser Ala Val Gly His Phe Thr Leu Gly Cys	
130 135 140	
gta ttg gaa gat caa gag cat caa gtc gct aaa gaa gaa agg gaa aca	480
Val Leu Glu Asp Gln Glu His Gln Val Ala Lys Glu Glu Arg Glu Thr	
145 150 155 160	
cct act act gat agt atg ccg cca tta tta cga caa gct atc gaa tta	528
Pro Thr Thr Asp Ser Met Pro Pro Leu Leu Arg Gln Ala Ile Glu Leu	
165 170 175	
ttt gat cac caa ggt gca gag cca gcc ttc tta ttc ggc ctt gaa ttg	576
Phe Asp His Gln Gly Ala Glu Pro Ala Phe Leu Phe Gly Leu Glu Leu	
180 185 190	

atc ata tgc gga tta gaa aaa caa ctt aaa tgt gaa agt ggg tcc gcg 624  
 Ile Ile Cys Gly Leu Glu Lys Gln Leu Lys Cys Glu Ser Gly Ser Ala  
 195 200 205

tac agc cgc gcg cgt acg aaa aac aat tac ggg tct acc atc gag ggc 672  
 Tyr Ser Arg Ala Arg Thr Lys Asn Asn Tyr Gly Ser Thr Ile Glu Gly  
 210 215 220

ctg ctc gat ctc ccg gac gac gac gcc ccc gaa gag gcg ggg ctg gcg 720  
 Leu Leu Asp Leu Pro Asp Asp Asp Ala Pro Glu Glu Ala Gly Leu Ala  
 225 230 235 240

gct ccg cgc ctg tcc ttt ctc ccc gcg gga cac acg cgc aga ctg tcg 768  
 Ala Pro Arg Leu Ser Phe Leu Pro Ala Gly His Thr Arg Arg Leu Ser  
 245 250 255

acg gcc ccc ccg acc gat gtc agc ctg ggg gac gag ctc cac tta gac 816  
 Thr Ala Pro Pro Thr Asp Val Ser Leu Gly Asp Glu Leu His Leu Asp  
 260 265 270

ggc gag gac gtg gcg atg gcg cat gcc gac gcg cta gac gat ttc gat 864  
 Gly Glu Asp Val Ala Met Ala His Ala Asp Ala Leu Asp Asp Phe Asp  
 275 280 285

ctg gac atg ttg ggg gac ggg gat tcc ccg ggt ccg gga ttt acc ccc 912  
 Leu Asp Met Leu Gly Asp Gly Asp Ser Pro Gly Pro Gly Phe Thr Pro  
 290 295 300

cac gac tcc gcc ccc tac ggc gct ctg gat atg gcc gac ttc gag ttt 960  
 His Asp Ser Ala Pro Tyr Gly Ala Leu Asp Met Ala Asp Phe Glu Phe  
 305 310 315 320

gag cag atg ttt acc gat ccc ctt gga att gac gag tac ggt ggg 1005  
 Glu Gln Met Phe Thr Asp Pro Leu Gly Ile Asp Glu Tyr Gly Gly  
 325 330 335

tag 1008

<210> 2  
 <211> 335  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> mutated Tn-10 derived Tet repressor

<400> 2  
 Met Ser Arg Leu Asp Lys Ser Lys Val Ile Asn Ser Ala Leu Glu Leu  
 1 5 10 15  
 Leu Asn Glu Val Gly Ile Glu Gly Leu Thr Thr Arg Lys Leu Ala Gln  
 20 25 30  
 Lys Leu Gly Val Glu Gln Pro Thr Leu Tyr Trp His Val Lys Asn Lys  
 35 40 45  
 Arg Ala Leu Leu Asp Ala Leu Ala Ile Glu Met Leu Asp Arg His His  
 50 55 60  
 Thr His Phe Cys Pro Leu Lys Gly Glu Ser Trp Gln Asp Phe Leu Arg  
 65 70 75 80  
 Asn Lys Ala Lys Ser Phe Arg Cys Ala Leu Leu Ser His Arg Asn Gly  
 85 90 95  
 Ala Lys Val His Ser Asp Thr Arg Pro Thr Glu Lys Gln Tyr Glu Thr  
 100 105 110

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```

Leu Glu Asn Gln Leu Ala Phe Leu Cys Gln Gln Gly Phe Ser Leu Glu
      115              120              125
Asn Ala Leu Tyr Ala Leu Ser Ala Val Gly His Phe Thr Leu Gly Cys
      130              135              140
Val Leu Glu Asp Gln Glu His Gln Val Ala Lys Glu Glu Arg Glu Thr
      145              150              155              160
Pro Thr Thr Asp Ser Met Pro Pro Leu Leu Arg Gln Ala Ile Glu Leu
      165              170              175
Phe Asp His Gln Gly Ala Glu Pro Ala Phe Leu Phe Gly Leu Glu Leu
      180              185              190
Ile Ile Cys Gly Leu Glu Lys Gln Leu Lys Cys Glu Ser Gly Ser Ala
      195              200              205
Tyr Ser Arg Ala Arg Thr Lys Asn Asn Tyr Gly Ser Thr Ile Glu Gly
      210              215              220
Leu Leu Asp Leu Pro Asp Asp Ala Pro Glu Glu Ala Gly Leu Ala
      225              230              235              240
Ala Pro Arg Leu Ser Phe Leu Pro Ala Gly His Thr Arg Arg Leu Ser
      245              250              255
Thr Ala Pro Pro Thr Asp Val Ser Leu Gly Asp Glu Leu His Leu Asp
      260              265              270
Gly Glu Asp Val Ala Met Ala His Ala Asp Ala Leu Asp Asp Phe Asp
      275              280              285
Leu Asp Met Leu Gly Asp Gly Asp Ser Pro Gly Pro Gly Phe Thr Pro
      290              295              300
His Asp Ser Ala Pro Tyr Gly Ala Leu Asp Met Ala Asp Phe Glu Phe
      305              310              315              320
Glu Gly Met Phe Thr Asp Pro Leu Gly His Asp Glu Tyr Gly Gly
      325              330              335

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<210> 3  
 <211> 33  
 <212> DNA  
 <213> Herpes simplex virus

<220>  
 <221> CDS  
 <222> (1)...(33)

<400> 3  
 gac gcg cta gac gat ttc gat ctg gac atg ttg

33

<210> 4  
 <211> 11  
 <212> PRT  
 <213> Herpes simplex virus

<400> 4  
 Asp Ala Leu Asp Asp Phe Asp Leu Asp Met Leu  
 1 5 10

<210> 5  
 <211> 7  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> nuclear localization signal

&lt;400&gt; 5

Met Pro Lys Arg Pro Arg Pro  
1 5

&lt;210&gt; 6

&lt;211&gt; 569

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Bidirectional promoter

&lt;400&gt; 6

```
gaattcgggg ccgcggaggc tggatcggtc ccggtgtctt ctatggaggt caaaacagcg 60
tggatggcgt ctccaggcga tctgacggtt cactaaacga gctctgctta tataggtcga 120
gtttaccact ccctatcagt gatagagaaa agtgaaagtc gagtttacca ctccctatca 180
gtgatagaga aaagtgaaag tcgagtttac cactccctat cagtgataga gaaaagtga 240
agtcgagttt accactccct accagtgata gagaaaagtg aaagtcgagt ttaccactcc 300
ctatcagtga tagagaaaag tgaaagtcga gtttaccact ccctatcagt gatagagaaa 360
agtgaaagtc gagtttacca ctccctatca gtgatagaga aaagtgaaag tcgagctcgg 420
taccggggtc gagtaggcgt gtacgggtgg aggcctatat aagcagagct cgtttagtga 480
accgtcagat cgccctggaga cgccatccac gctgttttga cctccataga agacaccggg 540
accgatccag cctccgcggc cccgaattc 569
```

&lt;210&gt; 7

&lt;211&gt; 520

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Bidirectional promoter

&lt;400&gt; 7

```
agatctgcag ggctcgctcg tgttcgaggc cacacgcgtc accttaatat gcgaagtgga 60
ccgatctcg agtttaccac tccctatcag tgatagagaa aagtgaaagt cgagtttacc 120
actccctatc agtgatagag aaaagtgaaa gtcgagttta ccaactcccta tcagtgatag 180
agaaaagtga aagtcgagtt taccactccc tatcagtgat agagaaaagt gaaagtcgag 240
tttaccactc cctatcagtg atagagaaaa gtgaaagtcg agtttaccac tccctatcag 300
tgatagagaa aagtgaaagt cgagtttacc actccctatc agtgatagag aaaagtgaaa 360
gtcgagctcg gtacccgggt cgagtaggcg tgtacgggtg gaggcctata taagcagagc 420
tcgtttagtg aaccgtcaga tcgcctggag acgccatcca cgctgttttg acctccatag 480
aagacaccgg gaccgatcca gcctccgcgg cccgaattc 520
```

&lt;210&gt; 8

&lt;211&gt; 450

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;221&gt; mRNA

&lt;222&gt; (382)...(450)

&lt;220&gt;

&lt;223&gt; Tetracycline-responsive PhCMV-1 promoter

&lt;400&gt; 8

```
gaattcctcg agtttaccac tccctatcag tgatagagaa aagtgaaagt cgagtttacc 60
actccctatc agtgatagag aaaagtgaaa gtcgagttta ccaactcccta tcagtgatag 120
agaaaagtga aagtcgagtt taccactccc tatcagtgat agagaaaagt gaaagtcgag 180
tttaccactc cctatcagtg atagagaaaa gtgaaagtcg agtttaccac tccctatcag 240
```

```

tgatagagaa aagtgaaagt cgagtttacc actccctatc agtgatagag aaaagtgaaa 300
gtcgaagctcg gtaccggggt cgagtaggcg tgtacgggtgg gaggcctata taagcagagc 360
tcgttttagtg aaccgtcaga tcgcctggag acgccatcca cgctgttttg acctccatag 420
aagacaccgg gaccgatcca gcctccgcgg                                450

```

&lt;210&gt; 9

&lt;211&gt; 450

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;221&gt; mRNA

&lt;222&gt; (382)...(450)

&lt;220&gt;

&lt;223&gt; Tet-regulated promoter

&lt;400&gt; 9

```

gaattcctcg acccggttac cgagctcgac tttcactttt ctctatcact gatagggagt 60
ggtaaaactcg actttcactt ttctctatca ctgataggga gtggtaaact cgactttcac 120
ttttctctat cactgatagg gagtggtaaa ctcgactttc acttttctct atcactgata 180
gggagtggtta aactcgactt tcaacttttct ctatcactga tagggagtgg taaactcgac 240
tttcaactttt ctctatcact gatagggagt ggtaaaactcg actttcactt ttctctatca 300
ctgataggga gtggtaaact cgagtaggcg tgtacgggtgg gaggcctata taagcagagc 360
tcgttttagtg aaccgtcaga tcgcctggag acgccatcca cgctgttttg acctccatag 420
aagacaccgg gaccgatcca gcctccgcgg                                450

```

&lt;210&gt; 10

&lt;211&gt; 398

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Herpes simplex virus minimal tk promoter linked to ten tet operator sequences

&lt;400&gt; 10

```

gagctcgact ttcacttttc tctatcactg atagggagtg gtaaaactcga ctttcacttt 60
tctctatcac tgataggagg tggtaaactc gactttcact tttctctatc actgataggg 120
agtggtaaact tcgactttca cttttctcta tcaactgatg ggagtggtta actcgacttt 180
cacttttctc tatcactgat agggagtggg aaactcgact ttcacttttc tctatcactg 240
atagggagtg gtaaaactcga ctttcacttt tctctatcac tgataggagg tggtaaactc 300
gagatccggc gaattcgaac acgcagatgc agtcggggcg gcgcgggtccg aggtccactt 360
cgcatattaa ggtgacgcgt gtggcctcga acaccgag                                398

```

&lt;210&gt; 11

&lt;211&gt; 38

&lt;212&gt; DNA

&lt;213&gt; Escherichia coli

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(38)

&lt;223&gt; class A tet operator

&lt;400&gt; 11

actttatcac tgataaaca acttatcagt gataaaga

38

&lt;210&gt; 12

&lt;211&gt; 38

&lt;212&gt; DNA

<213> Escherichia coli

<220>

<221> misc\_feature

<222> (1)...(38)

<223> class B tet operator

<400> 12

actctatcat tgatagagtt ccctatcagt gatagaga

38

<210> 13

<211> 38

<212> DNA

<213> Escherichia coli

<220>

<221> misc\_feature

<222> (1)...(38)

<223> class C tet operator

<400> 13

agcttatcat cgataagcta gtttatcaca gttaaatt

38

<210> 14

<211> 38

<212> DNA

<213> Escherichia coli

<220>

<221> misc\_feature

<222> (1)...(38)

<223> class D tet operator

<400> 14

actctatcat tgatagggaa ctctatcaat gataggga

38

<210> 15

<211> 38

<212> DNA

<213> Escherichia coli

<220>

<221> misc\_feature

<222> (1)...(38)

<223> Class E tet operator

<400> 15

aatctatcac tgatagagta ccctatcatc gatagaga

38

<210> 16

<211> 621

<212> DNA

<213> Escherichia coli

<220>

<221> misc\_feature

<222> (1)...(621)

<223> Tet repressor

<220>

<221> CDS

&lt;222&gt; (1)...(621)

&lt;400&gt; 16

atg tct aga tta gat aaa act aaa gtg att aac agc gca tta gag ctg	48
Met Ser Arg Leu Asp Lys Thr Lys Val Ile Asn Ser Ala Leu Glu Leu	
1 5 10 15	
ctt aat gag gtc gga atc gaa ggt tta aca acc cgt aaa ctc gcc cag	96
Leu Asn Glu Val Gly Ile Glu Gly Leu Thr Thr Arg Lys Leu Ala Gln	
20 25 30	
aag cta ggt gta gag cag cct aca ttg tat tgg cat gta aaa aat aag	144
Lys Leu Gly Val Glu Gln Pro Thr Leu Tyr Trp His Val Lys Asn Lys	
35 40 45	
cgg gct ttg ctc gac gcc tta gcc att gag atg tta gat agg cac cat	192
Arg Ala Leu Leu Asp Ala Leu Ala Ile Glu Met Leu Asp Arg His His	
50 55 60	
act cac ttt tgc cct tta gaa ggg gaa agc tgg caa gat ttt tta cgt	240
Thr His Phe Cys Pro Leu Glu Gly Glu Ser Trp Gln Asp Phe Leu Arg	
65 70 75 80	
aat aag gct aaa act ttt aga tgt gct tta cta agt cat cgc gat gga	288
Asn Lys Ala Lys Thr Phe Arg Cys Ala Leu Leu Ser His Arg Asp Gly	
85 90 95	
gca aaa gta cat tta ggt aca cgg cct aca gaa aaa cag tat gaa act	336
Ala Lys Val His Leu Gly Thr Arg Pro Thr Glu Lys Gln Tyr Glu Thr	
100 105 110	
ctc gaa aat caa tta gcc ttt tta tgc caa caa ggt ttt tca cta gag	384
Leu Glu Asn Gln Leu Ala Phe Leu Cys Gln Gln Gly Phe Ser Leu Glu	
115 120 125	
aat gca tta tat gca ctc agc gct gtg ggg cat ttt act tta ggt tgc	432
Asn Ala Leu Tyr Ala Leu Ser Ala Val Gly His Phe Thr Leu Gly Cys	
130 135 140	
gta ttg gaa gat caa gag cat caa gtc gct aaa gaa gaa agg gaa aca	480
Val Leu Glu Asp Gln Glu His Gln Val Ala Lys Glu Glu Arg Glu Thr	
145 150 155 160	
cct act act gat agt atg ccg cca tta tta cga caa gct atc gaa tta	528
Pro Thr Thr Asp Ser Met Pro Pro Leu Leu Arg Gln Ala Ile Glu Leu	
165 170 175	
ttt gat cac caa ggt gca gag cca gcc ttc tta ttc ggc ctt gaa ttg	576
Phe Asp His Gln Gly Ala Glu Pro Ala Phe Leu Phe Gly Leu Glu Leu	
180 185 190	
atc ata tgc gga tta gaa aaa caa ctt aaa tgt gaa agt ggg tcc	621
Ile Ile Cys Gly Leu Glu Lys Gln Leu Lys Cys Glu Ser Gly Ser	
195 200 205	

&lt;210&gt; 17

&lt;211&gt; 207



&lt;212&gt; PRT

&lt;213&gt; Escherichia coli

&lt;400&gt; 17

```

Met Ser Arg Leu Asp Lys Ser Lys Val Ile Asn Ser Ala Leu Glu Leu
 1          5          10          15
Leu Asn Glu Val Gly Ile Glu Gly Leu Thr Thr Arg Lys Leu Ala Gln
          20          25          30
Lys Leu Gly Val Glu Gln Pro Thr Leu Tyr Trp His Val Lys Asn Lys
          35          40          45
Arg Ala Leu Leu Asp Ala Leu Ala Ile Glu Met Leu Asp Arg His His
          50          55          60
Thr His Phe Cys Pro Leu Glu Gly Glu Ser Trp Gln Asp Phe Leu Arg
65          70          75          80
Asn Lys Ala Lys Ser Phe Arg Cys Ala Leu Ser His Arg Asp Gly
          85          90          95
Ala Lys Val His Leu Gly Thr Arg Pro Thr Glu Lys Gln Tyr Glu Thr
          100          105          110
Leu Glu Asn Gln Leu Ala Phe Leu Cys Gln Gln Gly Phe Ser Leu Glu
          115          120          125
Asn Ala Leu Tyr Ala Leu Ser Ala Val Gly His Phe Thr Leu Gly Cys
          130          135          140
Val Leu Glu Asp Gln Glu His Gln Val Ala Lys Glu Glu Arg Glu Thr
145          150          155          160
Pro Thr Thr Asp Ser Met Pro Pro Leu Leu Arg Ala His Glu Glu Leu
          165          170          175
Phe Asp His Gln Gly Ala Glu Pro Ala Phe Leu Phe Gly Leu Glu Leu
          180          185          190
Ile Ile Cys Gly Leu Glu Lys Gln Leu Lys Cys Glu Ser Gly Ser
          195          200          205

```

&lt;210&gt; 18

&lt;211&gt; 621

&lt;212&gt; DNA

&lt;213&gt; Escherichia coli

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (0)...(0)

&lt;223&gt; Mutated Tet repressor

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(621)

&lt;400&gt; 18

```

atg tct aga tta gat aaa agt aaa gtg att aac agc gca tta gag ctg      48
Met Ser Arg Leu Asp Lys Ser Lys Val Ile Asn Ser Ala Leu Glu Leu
 1          5          10          15

ctt aat gag gtc gga atc gaa ggt tta aca acc cgt aaa ctc gcc cag      96
Leu Asn Glu Val Gly Ile Glu Gly Leu Thr Thr Arg Lys Leu Ala Gln
          20          25          30

aag cta ggt gta gag cag cct aca ctg tat tgg cat gta aaa aat aag      144
Lys Leu Gly Val Glu Gln Pro Thr Leu Tyr Trp His Val Lys Asn Lys
          35          40          45

cgg gct ttg ctc gac gcc tta gcc att gag atg tta gat agg cac cat      192

```

Arg Ala Leu Leu Asp Ala Leu Ala Ile Glu Met Leu Asp Arg His His  
 50 55 60  
 act cac ttt tgc cct tta aaa ggg gaa agc tgg caa gat ttt tta cgc 240  
 Thr His Phe Cys Pro Leu Lys Gly Glu Ser Trp Gln Asp Phe Leu Arg  
 65 70 75 80  
 aat aag gct aaa agt ttt aga tgt gct tta cta agt cat cgc aat gga 288  
 Asn Lys Ala Lys Ser Phe Arg Cys Ala Leu Leu Ser His Arg Asn Gly  
 85 90 95  
 gca aaa gta cat tca gat aca cgg cct aca gaa aaa cag tat gaa act 336  
 Ala Lys Val His Ser Asp Thr Arg Pro Thr Glu Lys Gln Tyr Glu Thr  
 100 105 110  
 ctc gaa aat caa tta gcc ttt tta tgc caa caa ggt ttt tca cta gag 384  
 Leu Glu Asn Gln Leu Ala Phe Leu Cys Gln Gln Gly Phe Ser Leu Glu  
 115 120 125  
 aat gca tta tat gca ctc agc gct gtg ggg cat ttt act tta ggt tgc 432  
 Asn Ala Leu Tyr Ala Leu Ser Ala Val Gly His Phe Thr Leu Gly Cys  
 130 135 140  
 gta ttg gaa gat caa gag cat caa gtc gct aaa gaa gaa agg gaa aca 480  
 Val Leu Glu Asp Gln Glu His Gln Val Ala Lys Glu Glu Arg Glu Thr  
 145 150 155 160  
 cct act act gat agt atg ccg cca tta tta cga caa gct atc gaa tta 528  
 Pro Thr Thr Asp Ser Met Pro Pro Leu Leu Arg Gln Ala Ile Glu Leu  
 165 170 175  
 ttt gat cac caa ggt gca gag cca gcc ttc tta ttc ggc ctt gaa ttg 576  
 Phe Asp His Gln Gly Ala Glu Pro Ala Phe Leu Phe Gly Leu Glu Leu  
 180 185 190  
 atc ata tgc gga tta gaa aaa caa ctt aaa tgt gaa agt ggg tcc 621  
 Ile Ile Cys Gly Leu Glu Lys Gln Leu Lys Cys Glu Ser Gly Ser  
 195 200 205

&lt;210&gt; 19

&lt;211&gt; 207

&lt;212&gt; PRT

&lt;213&gt; Escherichia coli

&lt;400&gt; 19

Met Ser Arg Leu Asp Lys Ser Lys Val Ile Asn Ser Ala Leu Glu Leu  
 1 5 10 15  
 Leu Asn Glu Val Gly Ile Glu Gly Leu Thr Thr Arg Lys Leu Ala Gln  
 20 25 30  
 Lys Leu Gly Val Glu Gln Pro Thr Leu Tyr Trp His Val Lys Asn Lys  
 35 40 45  
 Arg Ala Leu Leu Asp Ala Leu Ala Ile Glu Met Leu Asp Arg His His  
 50 55 60  
 Thr His Phe Cys Pro Leu Lys Gly Glu Ser Trp Gln Asp Phe Leu Arg  
 65 70 75 80  
 Asn Lys Ala Lys Ser Phe Arg Cys Ala Leu Leu Ser His Arg Asn Gly  
 85 90 95  
 Ala Lys Val His Ser Asp Thr Arg Pro Thr Glu Lys Gln Tyr Glu Thr  
 100 105 110

```

Leu Glu Asn Gln Leu Ala Phe Leu Cys Gln Gln Gly Phe Ser Leu Glu
      115              120              125
Asn Ala Leu Tyr Ala Leu Ser Ala Val Gly His Phe Thr Leu Gly Cys
      130              135              140
Val Leu Glu Asp Gln Glu His Gln Val Ala Lys Glu Glu Arg Glu Thr
      145              150              155              160
Pro Thr Thr Asp Ser Met Pro Pro Leu Leu Arg Gln Ala Ile Glu Leu
      165              170              175
Phe Asp His Gln Gly Ala Glu Pro Ala Phe Leu Phe Gly Leu Glu Leu
      180              185              190
Ile Ile Cys Gly Leu Glu Lys Gln Leu Lys Cys Glu Ser Gly Ser
      195              200              205

```

<210> 20  
 <211> 192  
 <212> DNA  
 <213> *Drosophila melanogaster*

<220>  
 <221> misc\_feature  
 <222> (0)...(0)  
 <223> C64KR region

<220>  
 <221> CDS  
 <222> (1)...(192)

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<400> 20
gac atg gaa aaa gcg aca ccg gag acg atg gtc cat tgg att tgt ctg      48
Asp Met Glu Lys Ala Thr Pro Glu Thr Met Val His Trp Ile Cys Leu
  1              5              10              15

aag atg gag cca gct ctg tgg atg gcc att aca gca aca tcg cac ggc      96
Lys Met Glu Pro Ala Leu Trp Met Ala Ile Thr Ala Thr Ser His Gly
      20              25              30

gca agg cac agg aca ttc gtc ggg ttt tcc ggc tgc ctc cac cgc aaa      144
Ala Arg His Arg Thr Phe Val Gly Phe Ser Gly Cys Leu His Arg Lys
      35              40              45

tcc ctc acg tac cca gtg ata tgc ctg agc aaa ccg agc cag agg att      192
Ser Leu Thr Tyr Pro Val Ile Cys Leu Ser Lys Pro Ser Gln Arg Ile
  50              55              60

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<210> 21  
 <211> 64  
 <212> PRT  
 <213> *Drosophila melanogaster*

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<400> 21
Asp Met Glu Lys Ala Thr Pro Glu Thr Met Val His Trp Ile Cys Leu
  1              5              10              15
Lys Met Glu Pro Ala Leu Trp Met Ala Ile Thr Ala Thr Ser His Gly
      20              25              30
Ala Arg His Arg Thr Phe Val Gly Phe Ser Gly Cys Leu His Arg Lys
      35              40              45
Ser Leu Thr Tyr Pro Val Ile Cys Leu Ser Lys Pro Ser Gln Arg Ile
  50              55              60

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<210> 22  
 <211> 816  
 <212> DNA  
 <213> Avian erythroblastosis virus

<220>  
 <221> misc\_feature  
 <222> (1)...(816)  
 <223> v-erbA oncogene

<220>  
 <221> CDS  
 <222> (1)...(816)

<210> 22  
 <211> 816  
 <212> DNA  
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<220>  
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 <222> (1)...(816)

<221> misc\_feature  
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 <223> v-erbA oncogene

<400> 22  
 ctg gac gac tcg aag cgc gta gcc aag cgg aag ctg atc gag gag aac 48  
 Leu Asp Asp Ser Lys Arg Val Ala Lys Arg Lys Leu Ile Glu Glu Asn  
 1 5 10 15

cgg gag cgg cga cgc aag gag gag atg atc aaa tcc ctg cag cac cgg 96  
 Arg Glu Arg Arg Arg Lys Glu Glu Met Ile Lys Ser Leu Gln His Arg  
 20 25 30

ccc agc ccc agc gca gag gag tgg gag ctg atc cac gtg gtg acc gag 144  
 Pro Ser Pro Ser Ala Glu Glu Trp Glu Leu Ile His Val Val Thr Glu  
 35 40 45

gcg cac cgc agc acc aac gcg cag ggc agc cac tgg aag cag agg agg 192  
 Ala His Arg Ser Thr Asn Ala Gln Gly Ser His Trp Lys Gln Arg Arg  
 50 55 60

aaa ttc ctg ctc gaa gat atc ggt cag tcg ccc atg gcc tcc atg ctt 240  
 Lys Phe Leu Leu Glu Asp Ile Gly Gln Ser Pro Met Ala Ser Met Leu  
 65 70 75 80

gac ggg gac aaa gtg gac ctg gag gcg ttc agc gag ttt aca aaa atc 288  
 Asp Gly Asp Lys Val Asp Leu Glu Ala Phe Ser Glu Phe Thr Lys Ile  
 85 90 95

atc acg ccg gcc atc acc cgc gtg gtc gac ttt gcc aaa aac ctg ccc 336  
 Ile Thr Pro Ala Ile Thr Arg Val Val Asp Phe Ala Lys Asn Leu Pro  
 100 105 110

atg ttc tcg gag ctg ccg tgc gag gat cag atc atc ctg ctg aag ggc 384  
 Met Phe Ser Glu Leu Pro Cys Glu Asp Gln Ile Ile Leu Leu Lys Gly  
 115 120 125

tgc tgc atg gag atc atg tcg ctg cgc gcc gcc gtg cgc tac gac ccc	432
Cys Cys Met Glu Ile Met Ser Leu Arg Ala Ala Val Arg Tyr Asp Pro	
130 135 140	
 gag agc gaa acg ctg acg ctg agc ggg gaa atg gcc gtc aaa cgc gag	480
Glu Ser Glu Thr Leu Thr Leu Ser Gly Glu Met Ala Val Lys Arg Glu	
145 150 155 160	
 cag ttg aag aac gga ggg ctg ggg gtc gtg tct gat gcc atc ttc gac	528
Gln Leu Lys Asn Gly Gly Leu Gly Val Val Ser Asp Ala Ile Phe Asp	
165 170 175	
 ctc ggc aag tcg ctg tct gcc ttc aac ctg gac gac acc gag gtg gcc	576
Leu Gly Lys Ser Leu Ser Ala Phe Asn Leu Asp Asp Thr Glu Val Ala	
180 185 190	
 ctg ctg cag gcc gtg ctg ctc atg tcc tca gac cgg acg ggg ctg atc	624
Leu Leu Gln Ala Val Leu Leu Met Ser Ser Asp Arg Thr Gly Leu Ile	
195 200 205	
 tgc gtg gat aag ata gag aag tgc cag gag tcg tag ctg ctg gcg ttc	672
Cys Val Asp Lys Ile Glu Lys Cys Gln Glu Ser * Leu Leu Ala Phe	
210 215 220	
 gag cac tac atc aac tac cgc aaa cac aac att ccc cac ttc tgg tcc	720
Glu His Tyr Ile Asn Tyr Arg Lys His Asn Ile Pro His Phe Trp Ser	
225 230 235	
 aag ctg ctg atg aag gtg gcg gac ctg cgc atg atc ggc gcc tac cac	768
Lys Leu Leu Met Lys Val Ala Asp Leu Arg Met Ile Gly Ala Tyr His	
240 245 250 255	
 gcc agc cgc ttc ctg cac atg aag gtg gag tgc ccc acc gag ctc tcc	816
Ala Ser Arg Phe Leu His Met Lys Val Glu Cys Pro Thr Glu Leu Ser	
260 265 270	

&lt;210&gt; 23

&lt;211&gt; 272

&lt;212&gt; PRT

&lt;213&gt; Avian erythroblastosis virus

&lt;400&gt; 23

Leu Asp Asp Ser Lys Arg Val Ala Lys Arg Lys Leu Ile Glu Glu Asn	
1 5 10 15	
Arg Glu Arg Arg Arg Lys Glu Glu Met Ile Lys Ser Leu Gln His Arg	
20 25 30	
Pro Ser Pro Ser Ala Glu Glu Trp Glu Leu Ile His Val Val Thr Glu	
35 40 45	
Ala His Arg Ser Thr Asn Ala Gln Gly Ser His Trp Lys Gln Arg Arg	
50 55 60	
Lys Phe Leu Leu Glu Asp Ile Gly Gln Ser Pro Met Ala Ser Met Leu	
65 70 75 80	
Asp Gly Asp Lys Val Asp Leu Glu Ala Phe Ser Glu Phe Thr Lys Ile	
85 90 95	
Ile Thr Pro Ala Ile Thr Arg Val Val Asp Phe Ala Lys Asn Leu Pro	
100 105 110	
Met Phe Ser Glu Leu Pro Cys Glu Asp Gln Ile Ile Leu Leu Lys Gly	
115 120 125	
Cys Cys Met Glu Ile Met Ser Leu Arg Ala Ala Val Arg Tyr Asp Pro	
130 135 140	

Glu Ser Glu Thr Leu Thr Leu Ser Gly Glu Met Ala Val Lys Arg Glu  
 145 150 155 160  
 Gln Leu Lys Asn Gly Gly Leu Gly Val Val Ser Asp Ala Ile Phe Asp  
 165 170 175  
 Leu Gly Lys Ser Leu Ser Ala Phe Asn Leu Asp Asp Thr Glu Val Ala  
 180 185 190  
 Leu Leu Gln Ala Val Leu Leu Met Ser Ser Asp Arg Thr Gly Leu Ile  
 195 200 205  
 Cys Val Asp Lys Ile Glu Lys Cys Gln Glu Ser Tyr Leu Leu Ala Phe  
 210 215 220  
 Glu His Tyr Ile Asn Tyr Arg Lys His Asn Ile Pro His Phe Trp Ser  
 225 230 235 240  
 Lys Leu Leu Met Lys Val Ala Asp Leu Arg Met Ile Gly Ala Tyr His  
 245 250 255  
 Ala Ser Arg Phe Leu His Met Lys Val Glu Cys Pro Thr Glu Leu Ser  
 260 265 270

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 <212> DNA  
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<220>  
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<400> 24  
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25

<210> 25  
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 <212> DNA  
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<220>  
 <223> Polylinker

<400> 25  
 agtgggtccc cgggtgacat ggaa

24

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 <211> 8  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Polylinker

<400> 26  
 Ser Gly Ser Pro Gly Asp Met Glu  
 1 5

<210> 27  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Polylinker

<400> 27  
agtgggtccc cgggtctgga cgac

24

<210> 28  
<211> 8  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Polylinker

<400> 28  
Ser Gly Ser Pro Gly Leu Asp Asp  
1 5

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